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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 17, 2003, 11:18:03 ; Search time 1569.94 Seconds
(without alignments)
12007.805 Million cell updates/sec

Title: US-09-807-933B-10
Perfect score: 1164
Sequence: 1 atgaagtcacacgttcgtcat.....caggttcgcaagaagaa 1164

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 809774376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: em_estb1:*
2: em_estb2:*
3: em_estb3:*
4: em_estb4:*
5: em_estb5:*
6: em_estb6:*
7: em_estb7:*
8: em_estb8:*
9: em_estb9:*
10: em_estb10:*
11: em_estb11:*
12: em_estb12:*
13: em_estb13:*
14: em_estb14:*
15: em_estb15:*
16: em_estb16:*
17: em_estb17:*
18: em_estb18:*
19: em_estb19:*
20: em_estb20:*
21: em_estb21:*
22: em_estb22:*
23: em_estb23:*
24: em_estb24:*
25: em_estb25:*
26: em_estb26:*
27: em_estb27:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	173	14.9	691	10	BE585661 EST#6PSP6
2	122.2	10.5	450	13	BI200729 BI190695
3	111	9.5	444	13	BI190695 BI187295
4	104.4	9.0	426	13	BI187295 BI190568
5	81.2	7.0	215	13	BI190568 BI197365
6	73.6	6.3	989	17	CNS02H44 Tetradon

Result	Score	Query Match	Length	ID	Description
7	72	6.2	494	17	FR0048073
8	70.8	6.1	350	17	BH879665
9	70.6	6.1	450	17	PR0025683
10	70.6	6.1	501	17	FR0048173
11	70	6.0	914	17	AZ205202
12	69.6	6.0	933	17	AZ204694
13	67.8	5.8	788	17	AZ183942
14	67.2	5.8	627	17	BH179321
15	67.2	5.8	627	17	CNS071FL
16	66	5.7	735	17	CNS04NSM
17	65.8	5.7	335	10	AW275677
18	65.8	5.7	619	17	FR0047601
19	65.6	5.6	570	17	AZ149014
20	65.2	5.6	530	17	AZ166409
21	64.8	5.5	392	17	FR0048008
22	64.2	5.5	331	17	BH881398
23	64	5.5	500	17	B67199
24	63.8	5.5	354	17	AQ935615
25	63.4	5.4	250	17	BH878991
26	63.2	5.4	824	17	AZ185454
27	62.8	5.4	773	17	CNS01VTG
28	62.6	5.4	522	13	B1783235
29	62.6	5.4	621	17	AZ164800
30	62.2	5.3	358	17	BH777606
31	62.2	5.3	580	17	BH763893
32	62	5.3	177	17	BH881173
33	62	5.3	204	17	BH882682
34	62	5.3	230	17	BH869848
35	62	5.3	510	13	B0374789
36	62	5.3	619	17	FR0006944
37	62	5.3	810	17	AZ199472
38	61.8	5.3	218	17	BH875125
39	61.2	5.3	796	17	AZ186967
40	60.6	5.2	454	17	AZ178507
41	60.2	5.2	976	17	CNS01FBX
42	60	5.2	558	17	AZ146816
43	59.8	5.1	539	9	AT002510
44	59.6	5.1	485	13	B0370491
45	59.4	5.1	196	17	PR0047508

ALIGNMENTS

RESULT 1
BE585661
LOCUS
DEFINITION
EST#6PSP6 D02_d2_014 KSU wheat Fusarium graminearum infected spike
CDNA library Trilicium aestivum CDNA clone EST#6PSP6_D02_d2_014,
mRNA sequence.
ACCESSION
BE585661
VERSION
BE585661.1 GI:9838604
KEYWORDS
SOURCE
ORGANISM
Triticum aestivum
broad wheat.
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticeae; Triticum.
1 (bases 1 to 691)
REFERENCE
Fellers,J.P., Li,W.L., Hill-Ambroz,K., Matthews,A. and Gill,B.S.
The structure and function of the expressed portion of the wheat
genomes - Kansas State University. Fusarium graminearum infected
spike CDNA library
Unpublished (2000)
CONTACT
Contact: John Fellers
US Department of Agriculture, Agriculture Research Service, Plant
Science and Entomology Unit
Dept. of Plant Pathology, 4006 Throckmorton Hall, Kansas State
University, Manhattan, KS 66506, USA
Tel: 785-532-2367
Fax: 785-532-6167
Email: jpf@alfalfa.ksu.edu
Sequence have been trimmed to remove vector sequence and low

quality sequence with phred score less than 20
 Seg primer: SP6.
 Location/Qualifiers

FEATURES
 source

1. 691
 /organism="Triticum aestivum"
 /cultivar="Suma3"
 /db_xref="taxon:4565"
 /clone="EST6SP6 D02 d2 014"
 /clone_lib="KSU wheat Fusarium graminearum infected spike
 cDNA library"
 /tissue_type="Spike"
 /dev_stage="Adult plant"
 /lab_host="E. coli JM109"
 /note="Vector: pGEM-T easy; Site 1: SacII; Site 2: SpeI;
 plants were grown in the greenhouse. Spikes were sprayed
 with Fusarium graminearum (at what stage). Total RNA, and
 poly(A) RNA were prepared from infected spikes. cDNA was
 prepared using the SmartTM PCR cDNA synthesis kit from
 Clontech. cDNA was cloned into the pGEM-T easy vector
 from Promega."

BASE COUNT 135 a 196 c 163 g 197 t

ORIGIN

Query Match 14.9%; Score 173; DB 10; Length 691;
 Best Local Similarity 63.8%; Pred. No. 2.4e-39;
 Matches 279; Conservative 0; Mismatches 155; Indels 3; Gaps 1;

547 TCTGGAGTGGTTCACAACTGTTATGGATGTTGTAAGCTTCTTGAGCTGCT 606
 168 TCTGGAGTGGTTCACAACTGTTATGGATGTTGTAAGCTTCTTGAGCTGCT 227
 607 GGAAGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 666
 228 GGCAAGGCAAGTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 287
 667 GATGCCAATGCTCAAGTGGTGT--AACGGTGTATGGTTTCATGTATACAAAC 723
 288 AACCTGAAGCCGCTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 347
 724 CAACCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 783
 348 TCCCTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 407
 784 TCCACGAAGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 843
 408 GGCACTAGACACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 467
 844 TCTGGAAGAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 903
 468 AAGGGAAGAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 527
 904 TTGATTTGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 963
 528 TTTTACCTTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 587
 964 GCGCTCCCAATGATG 980
 588 GGCAAGCCCTCGGTG 604

RESULT 2
 BI200729 450 bp mRNA linear EST 10-JUL-2001
 LOCUS
 DEFINITION
 library Fusarium sporotrichioides cDNA clone olf05fs 5', mRNA
 sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

BI200729
 EST
 Fusarium sporotrichioides
 Fusarium sporotrichioides
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreales; mitosporic Hypocreales; Fusarium.

REFERENCE 1 (bases 1 to 450)
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

Ren Q., Tag A., Peplow A., Lai H., Kupfer C., Peterson A., Beremand
 M., and Roe B.
 Analysis of a Fusarium sporotrichioides EST database
 Unpublished (2001)
 Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
 Department of Chemistry and Biochemistry
 Advanced Center for Genome Technology, University of Oklahoma
 620 Parrington Oval, Norman, OK 73019, USA
 Tel: 405 325 4912
 Fax: 405 325 7762
 Email: broe@ou.edu
 Contact Dr. Marian Beremand regarding clone availability. Included
 is the best homolog from a blastx search of Genbank nr 04-09-01
 633 5e-66 94|1170140|sp|P45699 PUFATIVE ENDODUCCANASE TYPE
 KRECURSOR (EN
 Seq primer: T3
 High quality sequence step: 440.

FEATURES
 source

1. 450
 /organism="Fusarium sporotrichioides"
 /strain="Tri 10"
 /db_xref="taxon:5514"
 /clone="olf05fs"
 /clone_lib="Fusarium sporotrichioides Tri 10 overexpressed
 cDNA library"
 /note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
 XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript
 ; 3' end of cDNA cloned into XhoI site of pBluescript"

BASE COUNT 90 a 125 c 102 g 133 t

ORIGIN

Query Match 10.5%; Score 122.2; DB 13; Length 450;
 Best Local Similarity 63.6%; Pred. No. 1.5e-24;
 Matches 203; Conservative 0; Mismatches 113; Indels 3; Gaps 1;

547 TCTGGAGTGGTTCACAACTGTTATGGATGTTGTAAGCTTCTTGAGCTGCT 606
 132 TCTGGAGTGGTTCACAACTGTTATGGATGTTGTAAGCTTCTTGAGCTGCT 191
 607 GGAAGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 666
 192 GGCAAGGCAAGTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 251
 667 GATGCCAATGCTCAAGTGGTGTAA---CGTGTATGTTTCAATGTATACAAAC 723
 252 AACCTGAAGCCGCTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 311
 724 CAACCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 783
 312 TCCCTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 371
 784 TCCACGAAGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 843
 372 GGTATGAGGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 431
 844 TCTGGAAGAAGATGCTG 862
 432 AAGGCAAGAAGATGATG 450

RESULT 3
 BI190695 444 bp mRNA linear EST 10-JUL-2001
 LOCUS
 DEFINITION
 library Fusarium sporotrichioides cDNA clone i3g10fs 5', mRNA
 sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

BI190695
 EST
 Fusarium sporotrichioides
 Fusarium sporotrichioides
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

REFERENCE	Hypocreales; mitosporic Hypocreales; Fusarium.	
AUTHORS	Ren, Q., Tag, A., Peplow, A., Lai, H., Kupfer, C., Peterson, A., Beremand, M., and Roe, B.	
TITLE	Analysis of a Fusarium sporotrichioides EST database	
JOURNAL	Unpublished (2001)	
COMMENT	Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu Department of Chemistry and Biochemistry Advanced Center for Genome Technology, University of Oklahoma 620 Parrington Oval, Norman, OK 73019, USA Tel: 405 325 4912 Fax: 405 325 7762 Email: broe@ou.edu Contact Dr. Marian Beremand regarding clone availability Included is the bee. homolog from a blastx search of Genbank nr 04-09-01 576 3e-59 g1.1170140 sp P45699 PUTATIVE ENDOGLUCANASE TYPE KPRECURSOR (BN Seq primer: T3.	
FEATURES	Location/Qualifiers	
source	1..444 /organism="Fusarium sporotrichioides" /strain="Tti 10" /db_xref="taxon:5514" /clone="13g10fs" /clone_lib="Fusarium sporotrichioides Tti 10 overexpressed cDNA library" /note="vector: pBluescript SK-, site 1: EcoRI; site 2: XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript 3' end of cDNA cloned into XhoI site of pBluescript"	
BASE COUNT	85 a 127 c 92 g 140 t	
ORIGIN	Query Match 9.5%; Score 111; DB 13; Length 444; Bee Local Similarity 64.1%; Pred. No. 2.9e-21; Matches 184; Conservative 0; Mismatches 100; Indels 3; Gaps 1;	
Oy	547	TCGGCAGTGGTTCACACATCGTATTGGATTGTGTAAAGCTTCGACGCTGGCT 606
Db	158	TCTGGAAATGCGCACTCTACCTCGATCGATCGGACCTGCGCA3CCTTCCTGCTTGAGC 217
Oy	607	GGAAGAAGCTTCGATCAGTCGTCGTTGACACCTGTCGTCGCAATGGATCTTTATTA 666
Db	218	GCGAAGCTTAAGTCAGCGCCCTTGCTCTGACTTGTGCAADNAGATNACCTATCACT 277
Oy	667	GATGCCAATGCTCAAAAGTGTGTGA---CGGTGATAGGTTTCATGTGAACAAC 723
Db	278	AACCGAAGCGTGTCAACGTTGTGAGGCTGTGCTGTGCTGATGCTTGACCACTAC 337
Oy	724	CAACCTGGGCTGATCATGATGAGTGCCTTACGGTTGCGTGCCTCTATTGTGGC 783
Db	338	TCCCCGTGGGCTGTCAACGACACTTGCTTACGGTTGCGTGCACCAAGCTTGCGT 397
Oy	784	TCCAACGAAGCTGATGCTGTGTGCGCTGTATGAATTGACCTTAC 830
Db	398	GGTAGTAGGCGACGCTGGTGTGCTGTGCTATGCTTCACCTTCAC 444
RESULT 4		
LOCUS	B1187295 426 bp mRNA linear EST 10-JUL-2001	
DEFINITION	ath11fs.t1 Fusarium sporotrichioides Tti 10 overexpressed cDNA library Fusarium sporotrichioides cDNA clone ath11fs 5', mRNA sequence.	
ACCESSION	B1187295	
VERSION	B1187295.1 GI:14660974	
KEYWORDS	EST.	
SOURCE	Fusarium sporotrichioides.	
ORGANISM	Fusarium sporotrichioides.	
REFERENCE	Hypocreales; mitosporic Hypocreales; Fusarium.	
AUTHORS	Ren, Q., Tag, A., Peplow, A., Lai, H., Kupfer, C., Peterson, A., Beremand, M., and Roe, B.	

TITLE	COMMENT	BASE COUNT	ORIGIN
Analysis of a Fusarium sporotrichioides EST database	Unpublished (2001)		
Other ESTs: alh11f5.f1	Contact: Bruce A. Roe, University of Oklahoma, broeou.edu		
Contact: Bruce A. Roe, University of Oklahoma	Department of Chemistry and Biochemistry		
Advanced Center for Genome Technology, University of Oklahoma	620 Parrington Oval, Norman, OK 73019, USA		
Tel: 405 325 4912			
Fax: 405 325 7762	Email: broeou.edu		
Contact Dr. Marian Beremand regarding clone availability included	is the best homolog from a blastx search of Genbank nr 04-09-01		
565 56-58 g 11170140 ap P45699 PUTATIVE ENDOGLUCANASE TYPE	KREPCR5OR (EN		
Seq primer: T3			
High quality sequence stop: 338.			
Location/Qualifiers			
1. .426			
/organism="Fusarium sporotrichioides"			
/strain="Tri 10"			
/db_xref="taxon:5514"			
/clone="alh11f5"			
/cdna_lib="Fusarium sporotrichioides Tri 10 overexpressed			
/cdna_library"			
/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:			
XhoI; 5' end of CDNA cloned into EcoRI site of pBluescript			
; 3' end of CDNA cloned into XhoI site of pBluescript"			
82 a 119 c 91 g 134 t			
Query Match 9.0%; Score 104.4; DB 13; Length 426;			
Best Local Similarity 63.9%; Pred. No. 2.5e-19;			
Matches 175; Conservative 0; Mismatches 96; Indels 3; Gaps 1;			
OY	547 TCTGGAGGTGGTTCACACACCTGTTATGGATTGTGTAAAGCTTCGACGTGGCCT	606	
DB	148 TCTGGAAGTGGCCACTCTACTGATCTGGAGCTCTGCAGACCTTCTGCTTGGAGC	207	
OY	607 GGAAAGCTTGTCTGCTACTGTGCTGTGACACCTGTGCTCCAAATGATCTCTTTATTA	666	
DB	208 GGCAAGGTAAAGTCAGAGGCCCTGCTCTGATCTGTGACAAAGATTAACCTATCACT	267	
OY	667 GATGCCAATGCTCAAAGTGTGTA--CGGTGTATGTTTCATGATGTAAACACAC	723	
DB	268 AACCTGAACGCTGCAACGGTTGTGAGAGGTGTGTTCTGTTATGCTTGACCACTAC	327	
OY	724 CAACCTGGGGCTGCATGATGATGAGCTGCTTGAAGGTTTGGCTGTGCTCATTTGCTGGC	783	
DB	328 TCCCGTGGGGTGTCAACGACGACCTTGCTTACGTTTGGTCTGCTACCAAGCTTGCTGT	387	
OY	784 TCCACGAGAGCTGATGTGTTGTGGCTGTATG	817	
DB	388 GGTAGTGAGCGCACCTGTGTCTGTGCTTGTATG	421	
RESULT 5			
LOCUS	BI190568		
DEFINITION	215 bp mRNA linear EST 10-JUL-2001		
LOCUS	12a11f5.r1 Fusarium sporotrichioides Tri 10 overexpressed CDNA		
DEFINITION	library Fusarium sporotrichioides CDNA clone 12a11f5 5', mRNA		
DEFINITION	sequence.		
ACCESSION	BI190568		
VERSION	BI190568.1		
KEYWORDS	GI:14664247		
SOURCE	EST.		
ORGANISM	Fusarium sporotrichioides.		
ORGANISM	Fusarium sporotrichioides		
ORGANISM	Eukaryote; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;		
ORGANISM	Hypocreales; mitosporic Hypocreales; Fusarium.		
ORGANISM	1 (bases 1 to 215)		
ORGANISM	Ren.O., Tag.A., Peflow,A., Lai,H., Kuper,C., Peterson,A., Beremand		
ORGANISM	,M. and Roe,B.		
ORGANISM	Analysis of a Fusarium sporotrichioides EST database		
ORGANISM	Unpublished (2001)		

AUTHORS	CLARK, M. C.
TITLE	Direct Submission

sequence Location/Qualifiers

1.450
/organism="Takifugu rubripes"
/db_xref="taxon:31033"
/clone="154B17aC12"
/clone_11b="cosmid 154B17"

BASE COUNT 96 a 140 c 64 g 144 t 6 others

ORIGIN

Query Match 6.1%; Score 70.6; DB 17; Length 450;
Best Local Similarity 50.4%; Pred. No. 2.2e-09;
Matches 172; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

365 CTACAGACCAAGAGACATCTTCAAGACATCTACTACACCGCCAGGCTACTGCTA 424
78 CTACTACTACTACTGCTACTACTACTACTACTACTACTACTACTACTACTACTA 137
425 CTGTCCACCAAGACAGACATCAAGACATCAAGACATCAAGACATCAAGACATCA 484
138 CTGCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 197
485 CTGCGCGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 544
198 CTGCTGCTGCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 257
545 AATCTGCGAGTGTTCACAACTCGTTATTGGGATTGTGTAAGCTTCTTGACAGCTGC 604
258 CTACTGCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 317
605 CTGGAAGAGCTTCTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 664
318 CTATTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 377
665 TGATGCCAATGCTCAAGTGTGTTGTAAGCTGTTGTAAGTGT 705
378 CTGCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 418

RESULT 10
FR0048173 501 bp DNA linear GSS 05-JAN-2001
LOCUS
DEFINITION Fugu rubripes GSS sequence, clone 264E22cA9, genomic survey

ACCESSION AL444958.1 GI:12053458
VERSION AL444958.1
KEYWORDS GSS; genome survey sequence.
SOURCE Takifugu rubripes.
ORGANISM Takifugu rubripes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
Tetraodontidae; Takifugu.

REFERENCE
AUTHORS Clark, M.S.
TITLE Direct Submission
JOURNAL Submitted (29-SEP-2000) MRC Human Genome Mapping Project Resource
Centre Hinxton, Cambridge, CB10 1SB. UK Email:

COMMENT
biohelp@ngmp.mrc.ac.uk
Vector: pBluescript II KS
V type: phagemid
PRIMER: KS

DESCR: One pass dye-terminator sequencing of BAC (pBeloBAC11) cloned
genomic sequence
The BACS can be obtained from <http://www.incyte.com>.

FEATURES
source
1..501
/organism="Takifugu rubripes"
/db_xref="taxon:31033"
/clone="264E22cA9"
/clone_11b="BAC 264E22"

BASE COUNT 132 a 161 c 35 g 173 t

ORIGIN

Query Match 6.1%; Score 70.6; DB 17; Length 501;
Best Local Similarity 50.1%; Pred. No. 2.4e-09;
Matches 175; Conservative 0; Mismatches 174; Indels 0; Gaps 0;

354 TGCTGTAGCGTACAGACCAAGACATCTTCAAGACATCTACTACACCGCCCA 413
140 TGCTTCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 199
414 GGTACTGCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 473
200 TACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 259
474 GACTAGCACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 533
260 TACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 319
534 CTGCGCGGTAATCTGCGAGTGTTCACAACTCGTTATTGGGATTGTGTAAGCTTC 593
320 TTCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 379
594 TTGAGCTGGCGGTGGAAGCTTCTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTG 653
380 TACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 439
654 TATCTCTTATTAGATGCAATGCTCAAGTGTGTTGTAAGCTGTTAT 702
440 TGCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 488

RESULT 11
AZ205202 914 bp DNA linear GSS 31-AUG-2000
LOCUS
DEFINITION SP 0100 A2 G12 SP6E Strongylocentrotus purpuratus, purple sea
urchin, sperm genomic BAC library Strongylocentrotus purpuratus
genomic clone Plate=100 Col=24 Row=M, DNA sequence.

ACCESSION AZ205202.1 GI:8400122
VERSION AZ205202.1
KEYWORDS GSS.
SOURCE Strongylocentrotus purpuratus.
ORGANISM Strongylocentrotus purpuratus.
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida;
Strongylocentrotidae; Strongylocentrotus.

REFERENCE
AUTHORS Cameron, R.A., Mahitres, G., Rast, J.P., Martinez, P., Bondi, T.R.,
Sartwell, S., Wallace, J.C., Roushka, A.J., Livingston, B.T., Wray,
G.A., Eitensohn, C.A., Heinrich, H., Britten, R.J., Davidson, E.H. and
Hood, L.
A sea urchin genome project: Sequence scan, virtual map, and
additional resources
Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)

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MEDLINE
CONTACT: Cameron, RA, Davidson, EH, Hood, L
20402566
Division of Biology 156-29
California Institute of Technology
Pasadena California 91125, USA
Tel: (626) 395-8421
Fax: (626) 793-1047
Email: acameron@caltech.edu
Plate: 100 Row: M Column: 24
Seq primer: SP6
Class: BAC ends
High quality sequence stop: 914.

FEATURES
source
1..914
/organism="Strongylocentrotus purpuratus"
/db_xref="taxon:7668"
/clone="Plate=100 Col=24 Row=M"
/clone_11b="Strongylocentrotus purpuratus, purple sea
urchin, sperm genomic BAC library"
/note="Organ: sperm; Vector: BACs; 6; BAC clones in E-Coli

BASE COUNT 210 a 208 c 107 g 387 t 2 others
DH10B"

Query Match 6.0%; Score 70; DB 17; Length 914;
Best Local Similarity 48.7%; Pred. No. 5.6e-09;
Matches 190; Conservative 0; Mismatches 200; Indels 0; Gaps 0;

QY 346 AGTACAGAGCTGTGTAACGTGACGACCAAGACATCTACCAAGACTTACTACC 405
DB 169 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 228
QY 406 ACCGCAAGGCTACTGTGTAACGACCAAGACATCTACCAAGACTTACTACC 465
DB 229 ACCACACACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 288
QY 466 ACTACCAAGACTACTACTACTACTACTACTACTACTACTACTACTACTACT 525
DB 289 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 348
QY 526 AAGTATCTCTGGCGGTAAATCTGGAGGTTCACCAACTGTTATGGATTGTGT 585
DB 349 ACTGTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 408
QY 586 AAGCTTCTTGCGCTGCGCTGGAAGCTTGTGCTGCTGCTGCTGCTGCTGCTG 645
DB 409 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 468
QY 646 TCCATGTGATCTCTTTATTTAGATGCCATGCTCAAGTGTGAACGGTGTAAATG 705
DB 469 ACTAATGTGATGTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 528
QY 706 TTTATGTGTACCAACCAACCACTTGGGCT 735
DB 529 TTTGTATATATATATATATATATATGCTAGGT 558

RESULT 12
LOCUS AZ204694 933 bp DNA linear GSS 31-AUG-2000
DEFINITION SP 0100. A1 G12. SP68 Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library Strongylocentrotus purpuratus genomic clone Plate=100 Col=23 Row=M, DNA sequence.

ACCESSION AZ204694.1 GI:8399614
VERSION GSS.
KEYWORDS Strongylocentrotus purpuratus.
SOURCE Strongylocentrotus purpuratus
ORGANISM Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa; Echinoidea; Euechinoidea; Echinacea; Echinocida; Strongylocentrotidae; Strongylocentrotus.

REFERENCE 1 (bases 1 to 933)
AUTHORS Cameron, R.A., Mahliras, G., Rast, J.P., Martinez, P., Biondi, T.R., Swartzell, S., Wallace, J.C., Pousetka, A.J., Livingston, B.T., Wray, G.A., Etlensohn, C.A., Lehrach, H., Britten, R.J., Davidson, E.H. and Hood, L.

TITLE A sea urchin genome project: Sequence scan, virtual map, and additional resources
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)
MEDLINE 20402566
COMMENT Contact: Cameron, RA, Davidson, EH, Hood, L
Division of Biology 156-29
California Institute of Technology
Pasadena California 91125, USA
Tel: (626) 395-8421
Fax: (626) 793-3047
Email: acameron@caltech.edu
Plate: 100 Row: M Column: 23
Seq primer: SP6
Class: BAC ends
High quality sequence stop: 933.
Location/Qualifiers
1..933

FEATURES
source

/organism="Strongylocentrotus purpuratus"
/db_xref="taxon:7668"
/clone="Plate=100 Col=23 Row=M"
/clone_lib="Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library"
/note="Organ: sperm; Vector: BAC3.6; BAC Clones in E-Coli DH10B"

BASE COUNT 226 a 235 c 156 g 316 t
Query Match 6.0%; Score 69.6; DB 17; Length 933;
Best Local Similarity 48.9%; Pred. No. 7.4e-09;
Matches 186; Conservative 0; Mismatches 194; Indels 0; Gaps 0;

QY 336 CGATCCACAGTACAGTGTGTAACGCTAGACACCAAGACATCTACCAAGAC 395
DB 110 CGATACACCGGCAATCTACTACTACTACTACTACTACTACTACTACTACTACT 169
QY 396 ATCTACTACACCGGCAATCTACTACTACTACTACTACTACTACTACTACTACTACT 455
DB 170 TACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 229
QY 456 TACCAAGACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 515
DB 230 CACCACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 289
QY 516 TGTGTGTACAGGTATCTGGCGGTAAATCTGGAGGTTCACCAACTGTTATG 575
DB 290 TACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 349
QY 576 GATGTGTGAAGCTTGTGCGCTGCGCTGGAAGCTTGTGCTGCTGCTGCTGCTG 635
DB 350 TGTATATATTTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 409
QY 636 CACCTGTGCTCCATGTATCTTTATTTAGATGCCATGCTCAAGTGTGAACGG 695
DB 410 TACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 469
QY 696 TGTATGTGTTTCTATGTGTA 715
DB 470 TATAGTGTATGATTAATTATA 489

RESULT 13
LOCUS AZ183942 788 bp DNA linear GSS 30-AUG-2000
DEFINITION SP 1002. A1 H11. SP6 Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library Strongylocentrotus purpuratus genomic clone Plate=1002 Col=21 Row=O, DNA sequence.

ACCESSION AZ183942.1 GI:8356317
VERSION GSS.
KEYWORDS Strongylocentrotus purpuratus.
SOURCE Strongylocentrotus purpuratus
ORGANISM Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa; Echinoidea; Euechinoidea; Echinacea; Echinocida; Strongylocentrotidae; Strongylocentrotus.

REFERENCE 1 (bases 1 to 788)
AUTHORS Cameron, R.A., Mahliras, G., Rast, J.P., Martinez, P., Biondi, T.R., Swartzell, S., Wallace, J.C., Pousetka, A.J., Livingston, B.T., Wray, G.A., Etlensohn, C.A., Lehrach, H., Britten, R.J., Davidson, E.H. and Hood, L.

TITLE A sea urchin genome project: Sequence scan, virtual map, and additional resources
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COMMENT Contact: Cameron, RA, Davidson, EH, Hood, L
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California Institute of Technology
Pasadena California 91125, USA
Tel: (626) 395-8421
Fax: (626) 793-3047
Email: acameron@caltech.edu

FEATURES
source

to transform E. coli DH10B. The complete library contains 23808 clones from 4 independent sizing-ligation-transformations. Average insert size ranges from 70-127 kb and genome coverage is 7.9-fold.

FEATURES

Source

1. 627
 /organism="Schistosoma mansoni"
 /strain="Puerto-Rican"
 /db_xref="taxon:6183"
 /clone="014CH01"
 /clone_lib="SMBAC1"
 /note="end : T7"

BASE COUNT 169 a 79 c 196 g 167 t 16 others
 ORIGIN

Query Match

Best Local Similarity 52.3%; Score 67.2; DB 17; Length 627;
 Pred. No. 2.8e-08; Mismatches 118; Indels 0; Gaps 0;

Matches 135; Conservative 5; Mismatches 118; Indels 0; Gaps 0;

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QY 373 ACCAAGACATCTACCAAGACATCTACTACCGCCCAAGGCTACTGCTATCACC 432
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 398 ACGATTACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 339
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 433 ACCAAGACGTAACAAGACACTACCAAGACACTACCAAGACACTACGCGCT 492
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 338 ACTRCTACTGCTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 279
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 493 GCTTCTACTTCCACCTTCTTCTGCTGTACAGGTCACTCTGCGGTAAATCTGGC 552
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 278 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 219
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 553 AGTGTTCCACAACCTGTTATGGATGTTGTAAGCTTCTGCAGCTGCGCTGGA 612
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 218 ATTCTACTACMCCTACTCTSSCTTCTTCTACTATTTTGTAAACTGTACTAC 159
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 613 GCTTCTGTCACTGCTCT 630
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 158 AACCTGTCTACTGCTACT 141
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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 Job time : 1570.94 secs

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